CLAIM AMENDMENTS

In The Claims:

Claims 1-41. (Cancelled)

C1

42. (Currently Amended) A method of generating a variant comprising:

obtaining a nucleic acid comprising a sequence selected from the group consisting of SEQ ID NOS: 17, 18, 19, 20, ~~21,~~ 22, 23, ~~24, 35,~~and 39, sequences substantially identical thereto, sequences complementary thereto, fragments comprising at least 30 consecutive nucleotides thereof, and fragments comprising at least 30 consecutive nucleotides of the sequences complementary to SEQ ID NOS: 17, 18, 19, 20, ~~21,~~ 22, 23, ~~24, 35,~~and 39; and

modifying one or more nucleotides in said sequence to another nucleotide, deleting one or more nucleotides in said sequence, or adding one or more nucleotides to said sequence.

43. (Original) The method of claim 42, wherein the modifications are introduced by a method selected from the group consisting of error-prone PCR, shuffling, oligonucleotide directed mutagenesis, assembly PCR, sexual PCR mutagenesis, in viva mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, gene site saturated mutagenesis and any combination thereof

44. (Original) The method of claim 42, wherein the modifications are introduced by error-prone PCR.

45. (Original) The method of claim 42, wherein the modifications are introduced by shuffling.

46. (Original) The method of claim 42, wherein the modifications are introduced by oligonucleotide-directed mutagenesis.

47. (Original) The method of claim 42, wherein the modifications are introduced by assembly PCR.

48. (Original) The method of claim 42, wherein the modifications are introduced by sexual PCR mutagenesis.

49. (Original) The method of claim 42, wherein the modifications are introduced by in viva mutagenesis.

50. (Original) The method of claim 42, wherein the modifications are introduced by cassette mutagenesis.

51. (Original) The method of claim 42, wherein the modifications are introduced by recursive ensemble mutagenesis.

52. (Original) The method of claim 42, wherein the modifications are introduced by exponential ensemble mutagenesis.

53. (Original) The method of claim 42, wherein the modifications are introduced by site-specific mutagenesis.

54. (Original) The method of claim 42, wherein the modifications are introduced by gene reassembly.

55. (Original) The method of claim 42, wherein the modifications are introduced by gene site saturated mutagenesis.

Claims 56-92. (Cancelled)

93. (New) A method of generating a variant comprising:

obtaining a nucleic acid comprising a sequence encoding a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NOS:25, 26, 27, 28, 30, 31, and 40, sequences substantially identical thereto, sequences complementary thereto, fragments comprising at least 30 consecutive nucleotides thereof, and fragments comprising at least 30 consecutive nucleotides of the sequences complementary to SEQ ID NOS:25, 26, 27, 28, 30, 31, and 40; and

modifying one or more nucleotides in said sequence to another nucleotide, deleting one or more nucleotides in said sequence, or adding one or more nucleotides to said sequence.

94. (New) The method of claim 93, wherein the modifications are introduced by a method selected from the group consisting of error-prone PCR, shuffling, oligonucleotide directed mutagenesis, assembly PCR, sexual PCR mutagenesis, in viva mutagenesis, cassette mutagenesis, recursive ensemble mutagenesis, exponential ensemble mutagenesis, site-specific mutagenesis, gene reassembly, gene site saturated mutagenesis and any combination thereof